

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/08/842,827****TEAM 8**DATE: 09/11/97  
TIME: 11:39:07

INPUT SET: S20239.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

RECEIVED

SEP 25 1997

GROUP 1800

## (1) General Information:

(i) APPLICANT: LEUNG, David W.  
TOMPKINS, Christopher K.

(ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

(iii) NUMBER OF SEQUENCES: 21

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley & Lardner  
(B) STREET: 3000 K Street, N.W., Suite 500  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20007-5109

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/842,827  
(B) FILING DATE: 17-APR-1997  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BENT, Stephen A.  
(B) REGISTRATION NUMBER: 29,768  
(C) REFERENCE/DOCKET NUMBER: 77319/125

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202)672-5300  
(B) TELEFAX: (202)672-5399  
(C) TELEX: 904136

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1563 base pairs  
(B) TYPE: nucleic acid

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50
51
52      (ix) FEATURE:
53          (A) NAME/KEY: CDS
54          (B) LOCATION: 342..1193
55
56      (ix) FEATURE:
57          (A) NAME/KEY: mat_peptide
58          (B) LOCATION: 342..1193
59
60
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63      CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT      60
64
65      GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC      120
66
67      GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC      180
68
69      CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC      240
70
71      GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA      300
72
73      CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG      353
74                      Met Phe Asp Lys
75                      1
76
77      ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT      401
78      Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala
79      5                      10                      15                      20
80
81      GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA      449
82      Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg
83      25                      30                      35
84
85      GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC      497
86      Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp
87      40                      45                      50
88
89      ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT      545
90      Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile
91      55                      60                      65
92
93      ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG      593
94      Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu
95      70                      75                      80
96
97      CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA      641
98      His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys
99      85                      90                      95                      100

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100																	
101	GCC	ATT	GGA	ACC	TTT	TTA	TTT	GGT	GCA	GCT	GCT	AGT	CAG	TCC	CTG	ACT	689
102	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser	Gln	Ser	Leu	Thr	
103					105					110					115		
104																	
105	GAC	ATT	GCC	AAG	TAT	TCA	ATA	GGC	AGA	CTG	CGG	CCT	CAC	TTC	TTG	GAT	737
106	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	Asp	
107				120					125					130			
108																	
109	GTT	TGT	GAT	CCA	GAT	TGG	TCA	AAA	ATC	AAC	TGC	AGC	GAT	GGT	TAC	ATT	785
110	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	Asp	Gly	Tyr	Ile	
111			135					140					145				
112																	
113	GAA	TAC	TAC	ATA	TGT	CGA	GGG	AAT	GCA	GAA	AGA	GTT	AAG	GAA	GGC	AGG	833
114	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	Val	Lys	Glu	Gly	Arg	
115		150					155					160					
116																	
117	TTG	TCC	TTC	TAT	TCA	GGC	CAC	TCT	TCG	TTT	TCC	ATG	TAC	TGC	ATG	CTG	881
118	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	Tyr	Cys	Met	Leu	
119		165				170					175					180	
120																	
121	TTT	GTG	GCA	CTT	TAT	CTT	CAA	GCC	AGG	ATG	AAG	GGA	GAC	TGG	GCA	AGA	929
122	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	Asp	Trp	Ala	Arg	
123				185					190						195		
124																	
125	CTC	TTA	CGC	CCC	ACA	CTG	CAA	TTT	GGT	CTT	GTT	GCC	GTA	TCC	ATT	TAT	977
126	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	Ala	Val	Ser	Ile	Tyr	
127				200					205					210			
128																	
129	GTG	GGC	CTT	TCT	CGA	GTT	TCT	GAT	TAT	AAA	CAC	CAC	TGG	AGC	GAT	GTG	1025
130	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	Trp	Ser	Asp	Val	
131			215					220					225				
132																	
133	TTG	ACT	GGA	CTC	ATT	CAG	GGA	GCT	CTG	GTT	GCA	ATA	TTA	GTT	GCT	GTA	1073
134	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala	Ile	Leu	Val	Ala	Val	
135		230					235					240					
136																	
137	TAT	GTA	TCG	GAT	TTC	TTC	AAA	GAA	AGA	ACT	TCT	TTT	AAA	GAA	AGA	AAA	1121
138	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser	Phe	Lys	Glu	Arg	Lys	
139		245				250</											

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153 ACATAGTTAC CTTTAACTCA GTGGTTATCT AATAGCTCTA AACTCATTAA AAAA ACTCCA 1403  
154  
155 AGCCTTCCAC CAAAACAGTG CCCACCTGT ATACATTTT ATTAAAAAAA TGTAATGCTT 1463  
156  
157 ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTAA ATATAATACA 1523  
158  
159 TATTA AAATG TATGGGAGAA CCAAAAAAAA AAAAAAAAAA 1563  
160  
161

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

172  
173 Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys  
174 1 5 10 15  
175  
176 Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr  
177 20 25 30  
178  
179 Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro  
180 35 40 45  
181  
182 Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile  
183 50 55 60  
184  
185 Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr  
186 65 70 75 80  
187  
188 Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala  
189 85 90 95  
190  
191 Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser  
192 100 105 110  
193  
194 Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro  
195 115 120 125  
196  
197 His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser  
198 130 135 140  
199  
200 Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
201 145 150 155 160  
202  
203 Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
204 165 170 175  
205

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827

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206 Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
207      180      185      190
208
209 Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
210      195      200      205
211
212 Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
213      210      215      220
214
215 Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
216      225      230      235      240
217
218 Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
219      245      250      255
220
221 Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
222      260      265      270
223
224 Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
225      275      280
226

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 342..1196

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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247
248 CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT      60
249
250 GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC      120
251
252 GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC      180
253
254 CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC      240
255
256 GGGGCGGTCG CCAGCCCGGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCGCGA      300
257
258 CCTCATTTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG      353

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/842,827**

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*INPUT SET: S20239.raw*

Line

Error

Original Text